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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=10; day=10; hr=12; min=42; sec=39; ms=857;
]

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Application No: 10537839

Version No: 3.1

Input Set:

Output Set:

Started: 2008-10-10 12:40:22.231

Finished: 2008-10-10 12:40:28.906

Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 675 ms

Total Warnings: 36

Total Errors: 0

No. of SeqIDs Defined: 36

Actual SeqID Count: 36

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (15)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2008-10-10 12:40:22.231
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Total Warnings: 36
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Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)
W 213	Artificial or Unknown found in <213> in SEQ ID (35)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)

SEQUENCE LISTING

<110> Hart, Derek Nigel John
Kato, Masato

<120> DEC-205 (LY 75)/DCL-1 INTERGENIC SPLICE VARIANTS ASSOCIATED WITH HODGKIN'S
DISEASE, AND USES THEREOF

<130> DAVI257.002APC

<140> 10537839

<141> 2006-05-18

<150> PCT/AU03/01634

<151> 2003-12-05

<150> AU2002953223

<151> 2002-12-06

<160> 36

<170> PatentIn version 3.1

<210> 1

<211> 5622

<212> DNA

<213> mammalian

<220>

<221> CDS

<222> (1)..(5619)

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ctg ctc ttc tgg ttc ttc gat ctc gcg gag ccc tct ggc cgc gca gct	96
Leu Leu Phe Trp Phe Phe Asp Leu Ala Glu Pro Ser Gly Arg Ala Ala	
20 25 30	

aat gac ccc ttc acc atc gtc cat gga aat acg ggc aag tgc atc aag	144
Asn Asp Pro Phe Thr Ile Val His Gly Asn Thr Gly Lys Cys Ile Lys	
35 40 45	

cca gtg tat ggc tgg ata gta gca gac gac tgt gat gaa act gag gac	192
Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp	
50 55 60	

aag tta tgg aag tgg gtg tcc cag cat cgg ctc ttt cat ttg cac tcc	240
Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser	
65 70 75 80	

caa aag tgc ctt ggc ctc gat att acc aaa tcg gta aat gag ctg aga	288
Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg	

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100	105	110	
cac tct ctg tac gga gct gcc cgg	tac cgg ctg gct ctg aag gat gga		384
His Ser Leu Tyr Gly Ala Ala Arg	Tyr Arg Leu Ala Leu Lys Asp Gly		
115	120	125	
cat ggc aca gca atc tca aat gca	tct gat gtc tgg aag aaa gga ggc		432
His Gly Thr Ala Ile Ser Asn Ala	Ser Asp Val Trp Lys Lys Gly Gly		
130	135	140	
tca gag gaa agc ctt tgt gac cag	cct tat cat gag atc tat acc aga		480
Ser Glu Glu Ser Leu Cys Asp Gln	Pro Tyr His Glu Ile Tyr Thr Arg		
145	150	155	160
gat ggg aac tct tat ggg aga cct	tgt gaa ttt cca ttc tta att gat		528
Asp Gly Asn Ser Tyr Gly Arg Pro	Cys Glu Phe Pro Phe Leu Ile Asp		
165	170	175	
ggg acc tgg cat cat gat tgc att	ctt gat gaa gat cat agt ggg cca		576
Gly Thr Trp His His Asp Cys Ile	Leu Asp Glu Asp His Ser Gly Pro		
180	185	190	
tgg tgt gcc acc acc tta aat tat	gaa tat gac cga aag tgg ggc atc		624
Trp Cys Ala Thr Thr Leu Asn Tyr	Glu Tyr Asp Arg Lys Trp Gly Ile		
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tgc tta aag cct gaa aac ggt tgt	gaa gat aat tgg gaa aag aac gag		672
Cys Leu Lys Pro Glu Asn Gly Cys	Glu Asp Asn Trp Glu Lys Asn Glu		
210	215	220	
cag ttt gga agt tgc tac caa ttt	aat act cag acg gct ctt tct tgg		720
Gln Phe Gly Ser Cys Tyr Gln Phe	Asn Thr Gln Thr Ala Leu Ser Trp		
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aaa gaa gct tat gtt tca tgt cag	aat caa gga gct gat tta ctg agc		768
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245	250	255	
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Ile Asn Ser Ala Ala Glu Leu Thr	Tyr Leu Lys Glu Lys Glu Gly Ile		
260	265	270	
gct aag att ttc tgg att ggt tta	aat cag cta tac tct gct aga ggc		864
Ala Lys Ile Phe Trp Ile Gly Leu	Asn Gln Leu Tyr Ser Ala Arg Gly		
275	280	285	
tgg gaa tgg tca gac cac aaa cca	tta aac ttt ctc aac tgg gat cca		912
Trp Glu Trp Ser Asp His Lys Pro	Leu Asn Phe Leu Asn Trp Asp Pro		
290	295	300	
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Asp	Arg	Pro	Ser	Ala	Pro	Thr	Ile	Gly	Gly	Ser	Ser	Cys	Ala	Arg	Met	
305					310					315					320	
gat	gct	gag	tct	ggc	ctg	tgg	cag	agc	ttt	tcc	tgt	gaa	gct	caa	ctg	1008
Asp	Ala	Glu	Ser	Gly	Leu	Trp	Gln	Ser	Phe	Ser	Cys	Glu	Ala	Gln	Leu	
				325					330					335		
ccc	tat	gtc	tgc	agg	aaa	cca	tta	aat	aat	aca	gtg	gag	tta	aca	gat	1056
Pro	Tyr	Val	Cys	Arg	Lys	Pro	Leu	Asn	Asn	Thr	Val	Glu	Leu	Thr	Asp	
			340					345				350				
gtc	tgg	aca	tac	tca	gat	acc	cgc	tgt	gat	gca	ggc	tgg	ctg	cca	aat	1104
Val	Trp	Thr	Tyr	Ser	Asp	Thr	Arg	Cys	Asp	Ala	Gly	Trp	Leu	Pro	Asn	
		355					360				365					
aat	gga	ttt	tgc	tat	ctg	ctg	gta	aat	gaa	agt	aat	tcc	tgg	gat	aag	1152
Asn	Gly	Phe	Cys	Tyr	Leu	Leu	Val	Asn	Glu	Ser	Asn	Ser	Trp	Asp	Lys	
	370					375				380						
gca	cat	gcg	aaa	tgc	aaa	gcc	ttc	agt	agt	gac	cta	atc	agc	att	cat	1200
Ala	His	Ala	Lys	Cys	Lys	Ala	Phe	Ser	Ser	Asp	Leu	Ile	Ser	Ile	His	
385					390					395					400	
tct	cta	gca	gat	gtg	gag	gtg	gtt	gtc	aca	aaa	ctc	cat	aat	gag	gat	1248
Ser	Leu	Ala	Asp	Val	Glu	Val	Val	Val	Thr	Lys	Leu	His	Asn	Glu	Asp	
				405				410					415			
atc	aaa	gaa	gaa	gtg	tgg	ata	ggc	ctt	aag	aac	ata	aac	ata	cca	act	1296
Ile	Lys	Glu	Glu	Val	Trp	Ile	Gly	Leu	Lys	Asn	Ile	Asn	Ile	Pro	Thr	
			420				425					430				
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Leu	Phe	Gln	Trp	Ser	Asp	Gly	Thr	Glu	Val	Thr	Leu	Thr	Tyr	Trp	Asp	
		435				440					445					
gag	aat	gag	cca	aat	gtt	ccc	tac	aat	aag	acg	ccc	aac	tgt	gtt	tcc	1392
Glu	Asn	Glu	Pro	Asn	Val	Pro	Tyr	Asn	Lys	Thr	Pro	Asn	Cys	Val	Ser	
	450					455				460						
tac	tta	gga	gag	cta	ggc	cag	tgg	aaa	gtc	caa	tca	tgt	gag	gag	aaa	1440
Tyr	Leu	Gly	Glu	Leu	Gly	Gln	Trp	Lys	Val	Gln	Ser	Cys	Glu	Glu	Lys	
465					470					475					480	
cta	aaa	tat	gta	tgc	aag	aga	aag	gga	gaa	aaa	ctg	aat	gac	gca	agt	1488
Leu	Lys	Tyr	Val	Cys	Lys	Arg	Lys	Gly	Glu	Lys	Leu	Asn	Asp	Ala	Ser	
				485				490					495			
tct	gat	aag	atg	tgt	cct	cca	gat	gag	ggc	tgg	aag	aga	cat	gga	gaa	1536
Ser	Asp	Lys	Met	Cys	Pro	Pro	Asp	Glu	Gly	Trp	Lys	Arg	His	Gly	Glu	
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acc	tgt	tac	aag	att	tat	gag	gat	gag	gtc	cct	ttt	gga	aca	aac	tgc	1584
Thr	Cys	Tyr	Lys	Ile	Tyr	Glu	Asp	Glu	Val	Pro	Phe	Gly	Thr			

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Arg Asp Val Asp Ser Cys Gly Glu Tyr Asn Trp Ala Thr Val Gly Gly			
	565	570	575
aga agg cgg gct gta acc ttt tcc aac tgg aat ttt ctt gag cca gct			1776
Arg Arg Arg Ala Val Thr Phe Ser Asn Trp Asn Phe Leu Glu Pro Ala			
	580	585	590
tcc ccg ggc ggc tgc gtg gct atg tct act gga aag tct gtt gga aag			1824
Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Ser Val Gly Lys			
	595	600	605
tgg gag gtg aag gac tgc aga agc ttc aaa gca ctt tca att tgc aag			1872
Trp Glu Val Lys Asp Cys Arg Ser Phe Lys Ala Leu Ser Ile Cys Lys			
	610	615	620
aaa atg agt gga ccc ctt ggg cct gaa gaa gca tcc cct aag cct gat			1920
Lys Met Ser Gly Pro Leu Gly Pro Glu Glu Ala Ser Pro Lys Pro Asp			
625	630	635	640
gac ccc tgt cct gaa ggc tgg cag agt ttc ccc gca agt ctt tct tgt			1968
Asp Pro Cys Pro Glu Gly Trp Gln Ser Phe Pro Ala Ser Leu Ser Cys			
	645	650	655
tat aag gta ttc cat gca gaa aga att gta aga aag agg aac tgg gaa			2016
Tyr Lys Val Phe His Ala Glu Arg Ile Val Arg Lys Arg Asn Trp Glu			
	660	665	670
gaa gct gaa cga ttc tgc caa gcc ctt gga gca cac ctt tct agc ttc			2064
Glu Ala Glu Arg Phe Cys Gln Ala Leu Gly Ala His Leu Ser Ser Phe			
	675	680	685
agc cat gtg gat gaa ata aag gaa ttt ctt cac ttt tta acg gac cag			2112
Ser His Val Asp Glu Ile Lys Glu Phe Leu His Phe Leu Thr Asp Gln			
	690	695	700
ttc agt ggc cag cat tgg ctg tgg att ggt ttg aat aaa agg agc cca			2160
Phe Ser Gly Gln His Trp Leu Trp Ile Gly Leu Asn Lys Arg Ser Pro			
705	710	715	720
gat tta caa gga tcc tgg caa tgg agt gat cgt aca cca gtg tct act			2208
Asp Leu Gln Gly Ser Trp Gln Trp Ser Asp Arg Thr Pro Val Ser Thr			
	725	730	735
att atc atg cca aat gag ttt cag cag gat tat gac atc aga gac tgt			2256
Ile Ile Met Pro Asn Glu Phe Gln Gln Asp Tyr Asp Ile Arg Asp Cys			
	740	745	750
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Ala Ala Val Lys Val Phe His Arg Pro Trp Arg Arg Gly Trp His Phe	
755	760 765
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Tyr Asp Asp Arg Glu Phe Ile Tyr Leu Arg Pro Phe Ala Cys Asp Thr	
770	775 780
aaa ctt gaa tgg gtg tgc caa att cca aaa ggc cgt act cca aaa aca	2400
Lys Leu Glu Trp Val Cys Gln Ile Pro Lys Gly Arg Thr Pro Lys Thr	
785	790 795 800
cca gac tgg tac aat cca gac cgt gct gga att cat gga cct cca ctt	2448
Pro Asp Trp Tyr Asn Pro Asp Arg Ala Gly Ile His Gly Pro Pro Leu	
805	810 815
ata att gaa gga agt gaa tat tgg ttt gtt gct gat ctt cac cta aac	2496
Ile Ile Glu Gly Ser Glu Tyr Trp Phe Val Ala Asp Leu His Leu Asn	
820	825 830
tat gaa gaa gcc gtc ctg tac tgt gcc agc aat cac agc ttt ctt gcg	2544
Tyr Glu Glu Ala Val Leu Tyr Cys Ala Ser Asn His Ser Phe Leu Ala	
835	840 845
act ata aca tct ttt gtg gga cta aaa gcc atc aaa aac aaa ata gca	2592
Thr Ile Thr Ser Phe Val Gly Leu Lys Ala Ile Lys Asn Lys Ile Ala	
850	855 860
aat ata tct ggt gat gga cag aag tgg tgg ata aga att agc gag tgg	2640
Asn Ile Ser Gly Asp Gly Gln Lys Trp Trp Ile Arg Ile Ser Glu Trp	
865	870 875 880
cca ata gat gat cat ttt aca tac tca cga tat cca tgg cac cgc ttt	2688
Pro Ile Asp Asp His Phe Thr Tyr Ser Arg Tyr Pro Trp His Arg Phe	
885	890 895
cct gtg aca ttt gga gag gaa tgc ttg tac atg tct gcc aag act tgg	2736
Pro Val Thr Phe Gly Glu Glu Cys Leu Tyr Met Ser Ala Lys Thr Trp	
900	905 910
ctt atc gac tta ggt aaa cca aca gac tgt agt acc aag ttg ccc ttc	2784
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915	920 925
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Lys Cys Phe Leu Lys Ile Lys Pro Val Ser Leu Thr Phe Ser Gln Ala	
965	970 975
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Thr Leu Trp Ile Gly Leu Arg	Trp Thr Ala Tyr Glu	Lys Ile Asn	
1010	1015	1020	
aaa tgg aca gat aac aga gag	ctg acg tac agt aac	ttt cac cca	3114
Lys Trp Thr Asp Asn Arg Glu	Leu Thr Tyr Ser Asn	Phe His Pro	
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His Phe Val Ser Leu Cys Gln	Lys Tyr Ser Glu Val	Lys Ser Arg	
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Gln Thr Leu Gln Asn Ala Ser	Glu Thr Val Lys Tyr	Leu Asn Asn	
1100	1105	1110	
ctg tac aaa ata atc cca aag	act ctg act tgg cac	agt gct aaa	3384
Leu Tyr Lys Ile Ile Pro Lys	Thr Leu Thr Trp His	Ser Ala Lys	
1115	1120	1125	
agg gag tgt ctg aaa agt aac	atg cag ctg gtg agc	atc acg gac	3429
Arg Glu Cys Leu Lys Ser Asn	Met Gln Leu Val Ser	Ile Thr Asp	
1130	1135	1140	
cct tac cag cag gca ttc ctc	agt gtg cag gcg ctc	ctt cac aac	3474
Pro Tyr Gln Gln Ala Phe Leu	Ser Val Gln Ala Leu	Leu His Asn	
1145	1150	1155	
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Ser Ser Leu Trp Ile Gly Leu	Phe Ser Gln Asp Asp	Glu Leu Asn	
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Phe Gly Trp Ser Asp Gly Lys	Arg Leu His Phe Ser	Arg Trp Ala	
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1190 1195 1200

gga ttc tgg aaa aca gtt gat tgc aat gac aat caa cca ggt gct 3654
Gly Phe Trp Lys Thr Val Asp Cys Asn Asp Asn Gln Pro Gly Ala
1205 1210 1215

att tgc tac tat tca gga aat gag act ga